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Development of a novel nomogram for patients with SCLC and comparison with other models

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Abstract

Background Though several nomograms have been established to predict the survival probability of patients with small-cell lung cancer (SCLC), none involved enough variables. This study aimed to construct a novel prognostic nomogram and compare its performance with other models.

Methods Seven hundred twenty-two patients were pathologically diagnosed with SCLC in Shanxi Province Cancer Hospital, Shanxi Hospital Affiliated to Cancer Hospital, Chinese Academy of Medical Sciences, Cancer Hospital Affiliated to Shanxi Medical University from January 2016 to December 2018. We input Forty-one factors by reviewing the medical records. The nomogram was constructed based on the variables identified by univariate and multivariate analyses in the training set and validated in the validation set. Then we compared the performance of the models in terms of discrimination, calibration, and clinical net benefit.

Results There were eight variables involved in the nomogram: gender, monocyte (MON), neuron-specific enolase (NSE), cytokeratin 19 fragments (Cyfra211), M stage, radiotherapy (RT), chemotherapy cycles (CT cycles), and prophylactic cranial irradiation (PCI). The calibration curve showed a good correlation between the nomogram prediction and actual observation for overall survival (OS). The area under the curve (AUC) of the nomogram was higher, and the Integrated Brier score (IBS) was lower than other models, indicating a more accurate prediction. Decision curve analysis (DCA) showed a significant improvement in the clinical net benefit compared to the other models.

Conclusions We constructed a novel nomogram to predict OS for patients with SCLC using more comprehensive and objective variables. It performed better than existing models and would assist clinicians in individually estimating risk and making a therapeutic regimen.

Keywords (SCLC, Nomogram, Overall survival, Prediction, Individually treatment)

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Introduction

In China and throughout the world, lung cancer continues to be the leading cause of cancer-related death. [1, 2]. Because of its aggressive clinical course and early metastases, small cell lung cancer (SCLC), which accounts for approximately 15% of all lung cancer, has a poor prognosis. Although there is a high initial response to chemotherapy, the median overall survival (OS) of most patients with SCLC is limited due to drug resistance and recurrence within one year after treatment [3]. The early accurate identification of patients with a high risk of progression and death is of great significance for making the most favorable treatment decisions. The American Joint Committee on Cancer (AJCC) 8th edition TNM staging system, proposed by the International Association for the Study of Lung Cancer [4, 5], is routinely used to assess the prognosis of SCLC patients. However, its predictive accuracy is worth further consideration as the prognosis varies widely among patients with the same tumor stage in practice.

Previous research has demonstrated that various clinical features (including sex, age, and disease staging), pretreatment hematological parameters, pretreatment conventional tumor markers (such as monocytes, neuron-specific enolase, and Cyfra 21−1), along with therapeutic strategies (like chemotherapy, radiotherapy, and prophylactic cranial irradiation), are significantly linked to the prognosis of patients with small cell lung cancer [6–8]. Furthermore, there is a consensus that utilizing a combination of prognostic indicators is more effective for survival prediction than relying on individual markers. Nomogram is a graphical format that integrates multiple prognostic factors to achieve a personalized prognosis score for each patient. Nomogram has been widely used in various types of tumor diseases and has been proven more precise in predicting clinical outcomes [9–12]. Several prediction models in SCLC have been available, such as the nomogram published by Wang et al. [13], Pan et al. [14], Xiao et al. [15], and Xie et al. [16]. and the non-nomogram predictive models include the Manchester score [17] and Spain score [18]. Wang et al. [13]. based on the National Cancer Database (NCDB) showed that age, gender, race, ethnicity, Charlson/Deyo score, 8th-edition TNM staging, treatment mode, and tendency are significantly related to SCLC patient prognosis. The comprehensive AUC of the model built based on these factors was 0.789. Pan et al. [14]. study results on 355 patients showed that the accuracy of combining age, N stage, M stage, pathological subtype, PLR, NSE, and CYFRA211 in predicting the prognosis of SCLC in 1–2 years is better than the AJCC 7th edition TNM staging and VALSG staging system. The analysis results of Xiao et al. [15]. on 643 patients showed that the C index of the model constructed by gender, insurance status, VALSG stage and treatment mode was 0.60. Xie et al. [16]. built models for the limited stage and extensive stages showed good prediction performance, with a consistency index of 0.73. They have provided useful predictive tools to assist physicians in individualizing healthcare. However, all of them have some shortcomings. The two non-nomogram models were based on outdated therapy regimens [17, 18]. Three nomograms did not include hematological parameters and conventional tumor markers [13, 15, 16]. Two did not use the latest AJCC 8th TNM classification [14, 15]. What's more, the Xie et al. [16]. model did not perform independent external validation, probably due to the limited sample size. The Pan et al. [14]. model was developed on a small patient series, and its data included patients with compound histological types of SCLC. The Wang et al. [13]. model confirmed different races' effects on clinical outcomes, which were unsuitable for the Chinese population.

This study aimed to identify OS prognostic factors for SCLC patients and develop a novel prognostic nomogram model based on more comprehensive variables for the Chinese population. This study also compared the predictive performance of the proposed model with other existing models in terms of discrimination, calibration, and decision curve analysis. The article is presented according to the TRIPOD reporting checklist.

Materials and methods

Patient population and ethics statement

We reviewed the medical records of all patients pathologically diagnosed as SCLC with the complete treatment process and follow-up data in Shanxi Province Cancer Hospital, Shanxi Hospital Affiliated to Cancer Hospital, Chinese Academy of Medical Sciences, Cancer Hospital Affiliated to Shanxi Medical University from January 2015 to December 2018. All enrolled patients met the following criteria: (1) pathologically confirmed SCLC; (2) no history and concurrence of other malignant tumors; (3) no surgery; (4) no immunotherapy; (5) chemotherapy and/or radiotherapy; (6) complete clinicopathological and follow-up data. Finally, 722 cases without any missing value were enrolled in our study. Due to a lack of external validation, we divided the entire database into a training set (n=422) and a validation set (n=300) using a random seed count of 133. The selection process for enrolling patients is shown in Fig. 1.

This study received ethical approval from the Ethics committee of Shanxi Province Cancer Hospital, Shanxi Hospital Affiliated to Cancer Hospital, Chinese Academy of Medical Sciences, Cancer Hospital Affiliated to Shanxi Medical University (No. 202102). As this was a retrospective study and we hid all information about the patient's identity, the Ethics Committee waived informed consent.

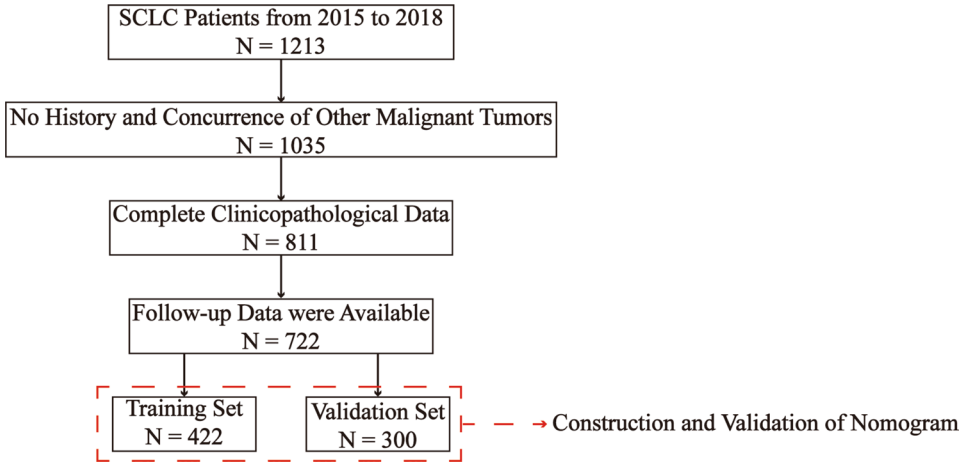

Fig. 1 Flow chart of patient selection in the training and validation set

The ethical criteria of the Declaration of Helsinki accompanied this study.

Data collection

We inputted variables from the following four aspects: clinical features (including age, gender, smoking history, smoking cessation, ECOG PS, tumor site, lymph node metastasis, pleural effusion, T stage, N stage, and M stage), pretreatment hematological parameters (white blood count, neutrophil, lymphocyte, monocyte, eosinophil, red blood cell, hemoglobin, hematocrit, mean corpuscular volume, mean corpuscular hemoglobin, mean corpuscular hemoglobin concentration, platelet, platelet distribution width, mean platelet volume, red cell distribution width, neutrophil to lymphocyte ratio, and platelet to lymphocyte ratio), pretreatment conventional tumor markers (carcinoma embryonic antigen, carbohydrate antigen 199, SCC, neuron-specific enolase, cytokeratin 19 fragments, pro-gastrin-releasing peptide, carbohydrate antigen 125, tissue polypeptide antigen, tissue polypeptide specific antigen, and vascular endothelial growth factor), and therapeutic strategies (radiotherapy, chemotherapy cycles, and prophylactic cranial irradiation). The clinical stage was based on the AJCC 8th edition TNM staging system and was determined by two senior chief physicians through the evaluation of enhanced computed tomography (CT) scans of the chest, abdomen, and pelvis, enhanced magnetic resonance imaging (MRI) of the head, and bone marrow examination. For hematological parameters and tumor markers, the laboratory's reference range was recorded as normal and the rest as abnormal. The Contala C' approach was adopted to define the threshold value of neutrophil to lymphocyte ratio (NLR), platelet to lymphocyte ratio (PLR), and red cell distribution width (RDW) [19], with the cut-off point for the NLR, PLR, and RDW at 3.9, 92 and 14.7, respectively. The therapeutic strategies include chemotherapy, radiotherapy (RT), and prophylactic cranial irradiation (PCI). We excluded the patients of surgical resection because the vast majority lost the chance of surgery due to the lymph nodes or distant metastases [20]. Those who have undergone surgery are usually at a very early stage, making up only a tiny proportion of SCLC patients, and tend to have good prognoses. We got patients' follow-up information by reviewing electronic medical records or contacting the patients directly. The last follow-up ended on August 20, 2020. Overall survival time was defined from the date of diagnosis to the date of death or the last follow-up.

Construction of the nomogram

The nomogram was constructed using 422 patients in the training set. Kaplan-Meier method was used to depict survival curves for all included variables, and the log-rank test was used to assess whether there was a statistical difference between groups. Variables with $P<0.05$ were included in a multivariate Cox regression model, with the smallest Akaike's information criterion (AIC) as the stopping rule [21, 22]. The final nomogram was built on the results of multivariate Cox regression analysis.

Validation of the nomogram

Based on the weight of each factor in the nomogram, the total score for each patient was calculated and used to depict the receiver-operating characteristics (ROC) curves. The AUC, which was close to the time-dependent ROC, was used to evaluate the predictive power of the nomogram. AUC was measured from 0.5 (random chance) to 1.0 (perfect discrimination), with a higher value indicating better prediction accuracy [23]. The calibration of the nomogram was evaluated by comparing the predicted probabilities with observed probabilities and plotting the calibration curve using 1,000 bootstrap resamples. The calibration curve of 45 degrees indicated

that the prediction model was perfect [23]. A distributional calibration (D-Calibration) determines whether a model's probability estimates are meaningful [24].

We compared the predictive accuracy of the proposed nomogram with TNM staging and other existing models using AUC in both the training and validation sets. Integrated Brier score (IBS) [25] and decision curve analyses (DCA) [26] were depicted to compare the calibration and the clinical net benefit, respectively.

Statistical analysis

The chi-squared test was used to compare categorical variables between the training and validation sets. Log-rank tests and multivariate analyses were used to select the optimal prognostic factors. All statistical analyses in this article were performed using R statistical software (version 3.6.3).

Results

Characteristics of patients

The baseline characteristics of SCLC patients are shown in Table 1. The median age at diagnosis was 61 years (range 23–82 years). The median follow-up time was 12.8 months, and 576 deaths (79.8% of the 722 totals) were observed. The median OS was 13.3 months, and the 1-, 2-, and 3-year OS rates were 54.2%, 24.9%, and 17%, respectively. All data were randomly divided into the training set (422) and validation set (300), and no statistically significant differences were found between the two groups, except ECOG PS and neuron-specific enolase (NSE).

Nomogram development and validation

In univariate and multivariate Cox regression analysis, eight variables were identified have a significant correlation with prognosis and were used to construct the nomogram, including gender, MON, NSE, Cyfra211, M stage, RT, CT cycles, and PCI (Table 2). The final nomogram model was established by integrating selected prognostic factors in the training set (Fig. 2), with an AUC of 0.881, 0.809, 0.790, 0.814, 0.813, and 0.815 at 6, 12, 18, 24, 30, and 36 months, respectively. Cross-validation also showed that the nomogram model had good predictive performance (Figure S1). The calibration plot showed an optimal agreement between the actual observed outcome and the nomogram-predicted OS (Fig. 3A). We further applied it to the validation group. The AUC of 0.840, 0.791, 0.779, 0.787, 0.807, and 0.841 at 6, 12, 18, 24, 30, and 36 months in the validation set, respectively. As shown in Fig. 3B, the calibration curves showed a good correlation between the nomogram prediction and actual observation for the OS. The *P* value for the five-fold cross-validation D-Calibration is 0.126. The results demonstrated that the nomogram we established was highly robust and accurate in predicting the prognosis of SCLC patients.

Comparison with 8th TNM staging and current prognostic model

As shown in Table 1, parameters forming part of the Wang et al. [13]. model and the Xiao et al. [15]. model such as race, occupation, health insurance were not considered in this study. It was, therefore, difficult to compare our model with these two models. More effort should be put into comparing our model and the 8th TNM staging, the Pan et al. [14]. model and the Xie et al. [16]. model. The predictive performance of the nomogram was assessed in terms of discrimination, calibration, and net benefit in both the training and validation sets. When compared with Xie et al. [16]. model, the entire database was divided into limited-stage SCLC (LS-SCLC) and extensive-stage SCLC (ES-SCLC) to make comparisons with the two nomograms proposed by Xie et al. [16].

The AUC was applied to quantify the discrimination. As shown in Fig. 4A and B, the proposed nomogram had a significantly higher AUC than the 8th TNM staging, the Pan et al. [14]. model, and the Xie et al. [16]. model in the majority of periods. Besides AUC, the Integrated Brier score (IBS) was also applied to evaluate the models' prediction performance by calculating each group's prediction error rate over time. The lower the IBS, the higher the predictive accuracy [25]. As shown in Fig. 5A and D, the IBS of the proposed nomogram for OS was lower than that of the AJCC 8th TNM staging system and the Pan et al. [14]. model in training and validation sets. In comparison with Xie et al. [16]. model, a similar result was observed in LS-SCLC (Fig. 5B and E) and ES-SCLC (Fig. 5C and F). Overall, our model had a lower error rate than the current models.

Decision curve analysis (DCA) [26] was performed to evaluate the clinical net benefit of the models. It revealed that in both the training and validation sets, the net benefit of the proposed nonogram was relatively higher compared to the AJCC 8th TNM staging system and the Pan et al., [14] model (Fig. 6A and D). When compared with Xie et al. [16]. model, Fig. 6B, C and E, and 6F showed a nearly similar clinical net benefit in both LS-SCLC and ES-SCLC.

Discussion

Though varieties of prognostic factors associated with SCLC have been identified and several prediction models have been proposed in earlier published studies, they need more variables to be developed specifically for the Chinese population. We constructed a nomogram based on 722 patients in a single institution, which contains as many variables as possible and performs better than other existing models. Meanwhile, we made a systematic

Table 1 Clinical features of the training and validation groups

Factors	Total ($n=722$)	Training set ($n=422$)	Validation set ($n=300$)	*P* value
Gender (Male/Female)	592/130	355/67	237/63	0.077
Age70 (< 70/≥70)	604/118	352/70	252/48	0.833
Smoke (Yes/No)	544/178	324/98	220/80	0.290
Smoking cessation (Yes/No)	277/445	162/260	115/185	0.988
ECOG PS (< 2/≥2)	591/131	330/92	261/39	0.002
Tumor site (Left side/Right side)	334/388	184/238	150/150	0.089
LN (Yes/No)	657/65	386/36	271/29	0.599
Pleural effusion (Yes/No)	281/441	163/259	118/182	0.848
WBC (Normal/Abnormal)	610/112	354/68	256/44	0.597
NEU (Normal/Abnormal)	581/141	340/82	241/59	0.937
LYM (Normal/Abnormal)	600/122	355/67	245/55	0.385
MON (Normal/Abnormal)	505/217	289/133	216/84	0.310
EOS (Normal/Abnormal)	662/60	386/36	276/24	0.799
RBC (Normal/Abnormal)	574/148	330/92	244/56	0.304
HGB (Normal/Abnormal)	481/241	283/139	198/102	0.766
HCT (Normal/Abnormal)	512/210	303/119	209/91	0.534
MCV (Normal/Abnormal)	637/85	373/49	264/36	0.873
MCH (Normal/Abnormal)	677/45	398/24	279/21	0.472
MCHC (Normal/Abnormal)	677/45	376/46	263/37	0.552
PLT (Normal/Abnormal)	578/144	340/82	238/62	0.682
PDW (Normal/Abnormal)	471/251	274/148	197/103	0.837
MPV (Normal/Abnormal)	486/236	277/145	209/91	0.256
CEA (Normal/Abnormal)	453/269	272/150	181/119	0.259
CA199 (Normal/Abnormal)	634/88	367/55	267/33	0.411
SCC (Normal/Abnormal)	690/32	401/21	289/11	0.399
NSE (Normal/Abnormal)	252/470	161/261	91/209	0.030
Cyfra211 (Normal/Abnormal)	618/107	366/56	252/48	0.303
ProGRP (Normal/Abnormal)	184/538	106/316	78/222	0.789
CA125 (Normal/Abnormal)	528/194	311/111	217/83	0.684
TPA (Normal/Abnormal)	497/225	301/121	196/104	0.087
TPS (Normal/Abnormal)	412/310	242/180	170/130	0.856
VEGF (Normal/Abnormal)	517/205	302/120	215/85	0.976
NLR (< 3.9/≥3.9)	553/169	322/100	231/69	0.828
RDW (< 14.7/≥14.7)	683/39	401/21	282/18	0.549
PLR (< 92/≥92)	536/186	314/108	222/78	0.902
T stage (T1/T2/T3/T4)	63/188/153/318	35/112/89/186	28/76/64/132	0.956
N stage (N0/N1/N2/N3)	54/19/315/334	33/9/187/193	21/10/128/141	0.732
M stage (M0/M1a/M1b/M1c)	423/86/52/161	259/50/31/82	164/36/21/79	0.163
RT (Yes/No)	287/435	176/246	111/189	0.203
CT cycles (< 4/≥4)	259/463	149/273	110/190	0.708
PCI (Yes/No)	66/656	45/377	21/279	0.092
Survival status (Alive/Dead)	146/576	89/333	57/243	0.491

Abbreviations ECOG PS, Eastern Cooperative Oncology Group performance score; LN, lymph node metastasis; WBC, white blood count; NEU, neutrophil; LYM, lymphocyte; MON, monocyte; EOS, eosinophil; RBC, red blood cell; HGB, hemoglobin; HCT, hematocrit; MCV, mean corpuscular volume; MCH, mean corpuscular hemoglobin; MCHC: mean corpuscular hemoglobin concentration; PLT, platelet; PDW, platelet distribution width; MPV, mean platelet volume; CEA, carcinoma embryonic antigen; CA199/ CA125, carbohydrate antigen; SCC, Squamous cell carcinoma associated antigen; NSE, neuron-specific enolase; Cyfra211, cytokeratin 19 fragments; ProGRP, pro-gastrin-releasing peptide; TPA, Tissue polypeptide antigen; TPS, Tissue Polypeptide Specific Antigen; VEGF, vascular endothelial growth factor; RT, radiotherapy; CT cycles, chemotherapy cycles; PCI, prophylactic cranial irradiation; NLR, neutrophil to lymphocyte ratio; PLR, platelet to lymphocyte ratio; RDW, red cell distribution width

assessment of these models. The results show that the proposed nomogram has higher discriminative power, better calibration and greater net benefit compared with the Pan et al. model and 8th TNM staging. Compared with the Xie et al. model, although the net benefit is similar, the time-dependent AUC shows that the proposed nomogram has a more stable and higher predictive performance. The proposed nomogram will enable survival probability estimation for making individualized

Table 2 The results of multivariate analysis based on the minimum AIC in the training set

Factors	HR (95%CI)	*P* value
Gender		
Female	Reference	
Male	1.386 (1.000-1.921)	0.050
NSE		
Normal	Reference	
Abnormal	1.412(1.110–1.796)	0.005
Cyfra211		
Normal	Reference	
Abnormal	2.021(1.478–2.763)	< 0.001
MON		
Normal	Reference	
Abnormal	1.294(1.025–1.633)	0.030
M stage		
M0	Reference	
M1a	1.091(0.769–1.547)	0.001
M1b	1.442(0.936–2.223)	
M1c	2.008(1.486–2.714)	
RT		
No	Reference	
Yes	0.750(0.574–0.980)	0.035
CT cycles		
< 4	Reference	
≥ 4	0.397(0.311–0.507)	< 0.001
PCI		
No	Reference	
Yes	0.418(0.256–0.682)	0.001

Abbreviations HR, hazard ratio; CI, confidence interval; MON, monocyte; NSE, neuron specific enolase; Cyfra211, cytokeratin 19 fragment; CT cycles, chemotherapy cycles; PCI, prophylactic cranial irradiation

treatment decisions and design and conduction of prospective clinical trials.

The proposed nomogram included conventional tumor markers such as NSE and Cyfra211 as independent predictors of outcomes in SCLC patients. Serum NSE is an acid protease specific to neurons and neuroendocrine cells, which is a specific marker of neuroendocrine tumors. It's reported that 80% of SCLC patients have elevated serum levels, which may be the most sensitive marker for diagnosing SCLC [27]. Recent research has confirmed that NSE is not only helpful in the diagnosis of SCLC but also helpful in evaluating the therapeutic effect and predicting patient outcomes [28]. It is acknowledged that Cyfra211 is a specific marker in non-small cell lung cancer (NSCLC) [29]. A recent study confirmed that Cyfra211 has the value of diagnosis and prediction not only in NSCLC but also in SCLC [30]. The change of Cyfra211 during therapy can indicate the efficacy of treatment earlier, which is vital to evaluate the prognosis of patients with SCLC.

In our study, neither the primary tumor (T) stage nor lymph node metastasis (N stage) was an independent prognostic factor except for distant metastasis (M stage) in patients with SCLC. All know that an increasing number of metastatic sites leads to a worse prognosis [31]. The T and N stages are generally determined by thorax CT scans, highly dependent on the radiologist's experience. The proposed nomogram didn't include T and N stages, significantly reducing subjectivity and variability.

Our results also showed the vital role of MON for prognosis in SCLC. It is generally examined that inflammation in the tumor microenvironment is a critical ingredient of cancer progression [32]. Monocyte in the blood is the predecessor of macrophages [33]. The chemokines produced in the tumor microenvironment induce MON to move

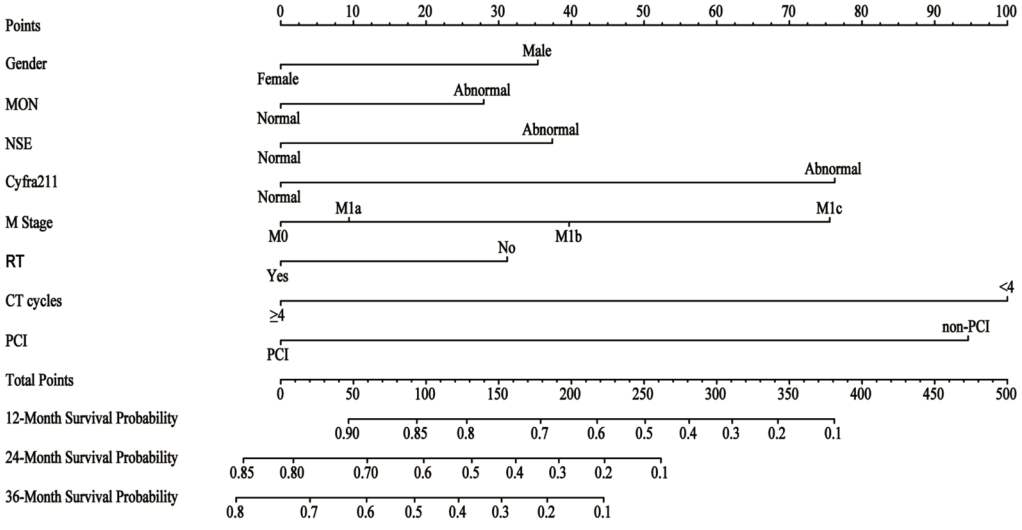

Fig. 2 Nomogram to predict 1, 2, and 3-year overall survival for patients with SCLC

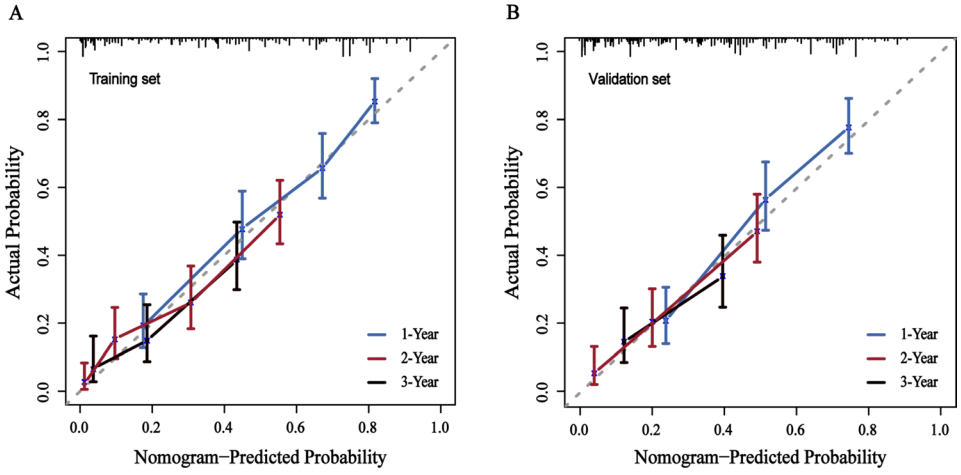

Fig. 3 The calibration curve of the nomogram for predicting survival probability in the training set (**A**) and validation set (**B**)

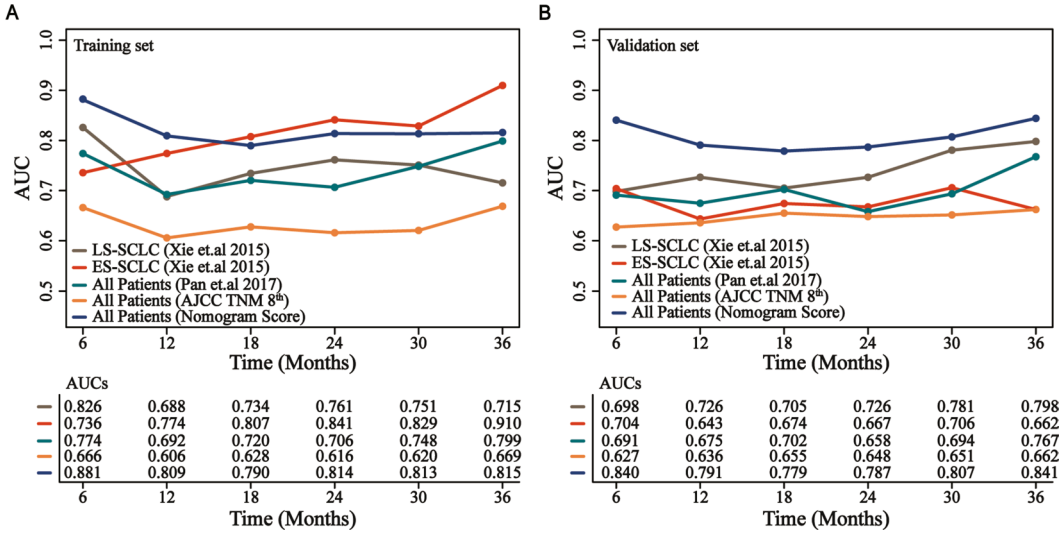

Fig. 4 The area under the receiver operating characteristic (ROC) curve (AUC) in the training set (**A**) and validation set (**B**)

to the tumor tissue. The cells infiltrated in tumor sites are called tumor-associated macrophages (TAMs) [34, 35], which significantly impact the development and progression of SCLC. Our study demonstrated that elevated MON substantially correlates with a worse prognosis.

The therapeutic regimen contributes the most to the OS of patients with SCLC. Although immunotherapy has become the new standard of first-line treatment for ES-SCLC in the Chinese Society of Clinical Oncology (CSCO) guideline in 2020.05, the number of patients undergoing immunotherapy in China is limited due to its high price. As atezolizumab has not been covered by Chinese health insurance, it will still be long before immunotherapy is widely used in clinical practice. Given that most patients with SCLC lose the opportunity of surgical resection due to the lymph nodes or distant metastases [20], platinum-based chemotherapy for 4–6 cycles remains the first-line standard treatment [36]. Our results demonstrate that patients who received chemotherapy in less than four cycles are associated with poor outcomes. In addition to chemotherapy cycles, thoracic radiotherapy also plays a vital role in improving the survival rate of SCLC patients, which is consistent with the results from Li et al. [37]. It is known that brain metastases (BM) are one of the most common sites of SCLC distant metastasis and usually result in a poor prognosis. PCI has been confirmed to reduce the incidence of brain metastases in both LS-SCLC and ES-SCLC [38]. The results of our study indicate patients without PCI are associated with poor outcomes.

The superior performance of the proposed nomogram has been verified in comparison with the existing models. Although the AUC of Xie's ES-SCLC model in the training set was higher than the model developed in our study at 16–36 months, there was no difference with IBS compared to the Xie et al. model [16] when predicting survival time for ES-SCLC patients over 15 months. It has

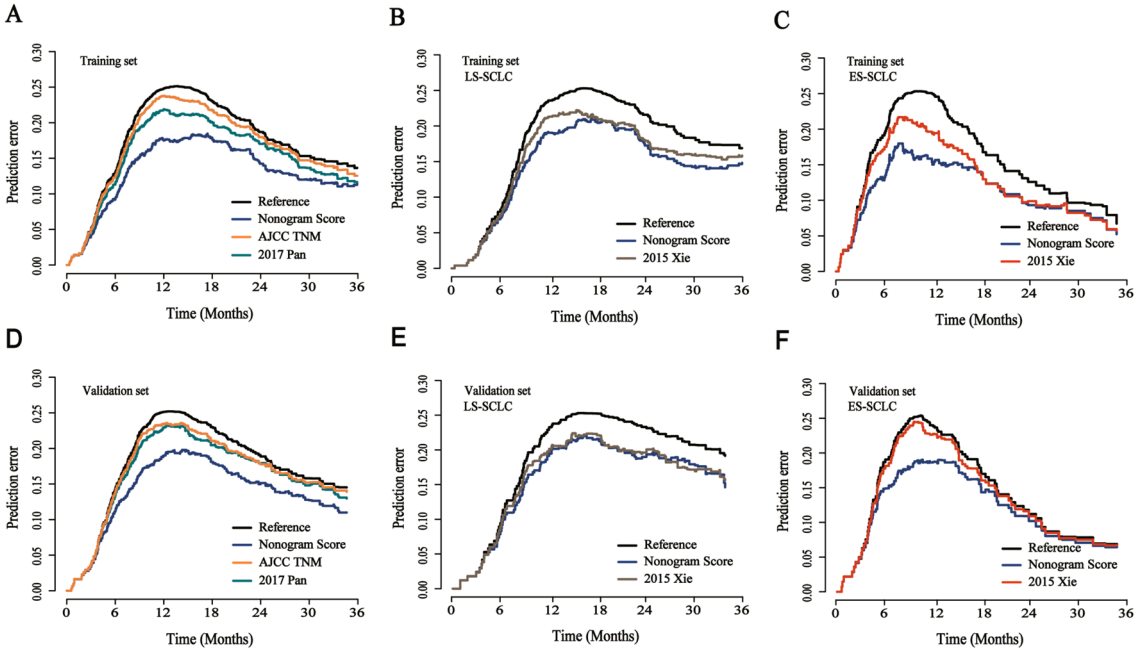

Fig. 5 The Integrated Brier score (IBS) in the training set and validation set

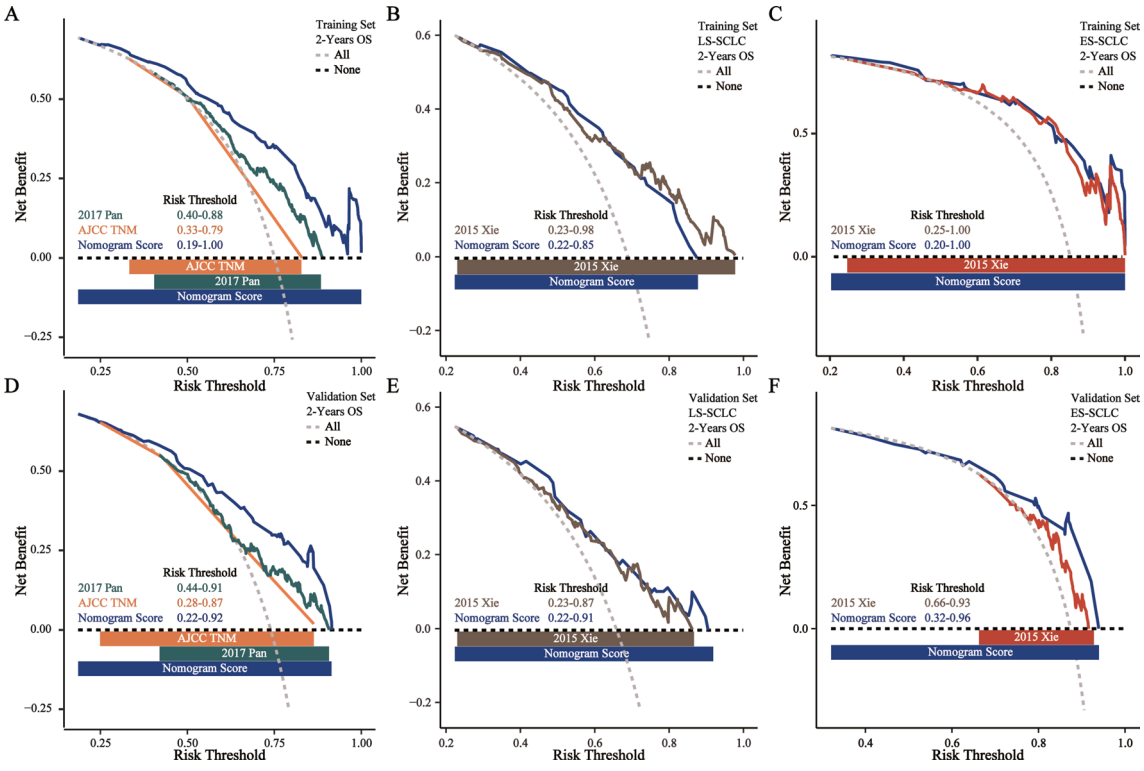

Fig. 6 Decision curve analysis (DCA) in the training set and validation set

been reported that the median survival of ES-SCLC was only 7–10 months [39], and most patients didn't live for 15 months. Similarly, from the supplementary material of Xie's study, we may deduce that only one in five patients with ES-SCLC in their study group lived for more than 15 months.

Despite the superior performance, there were several limitations in our study. First, the nomogram was constructed and validated internally in a single center.

Further validation in multiple institutions is needed. Secondly, we didn't enroll patients undergoing immunotherapy because the patients in our study were diagnosed with SCLC before 2019 when immunotherapy was not a first-line treatment for extensive SCLC. Third, we should have included variables such as comorbidity scores and gene mutation. Finally, the exclusion of molecular subtypes represents a significant limitation. Recent research has demonstrated that molecular subtypes, including ASCL1, NEUROD1, POU2F3, and YAP1, also substantially impact the prognosis of small-cell lung cancer and are being increasingly refined for use in clinical practice as a practical evaluation method [40]. Therefore, future research could integrate these molecular features to enhance the accuracy of prognostic assessments, thereby improving personalized treatment strategies and ultimately providing more precise treatment options for patients.

Conclusions

In conclusion, we have constructed a new nomogram to predict OS using more comprehensive and objective variables for SCLC in China, which have been proven to perform better than TNM Staging and other prognostic models. The proposed nomogram also provides an easy and optimal tool for clinicians to individually estimate the risk and make therapeutic regimens for patients with SCLC.

Supplementary Information

The online version contains supplementary material available at https://doi.org/10.1186/s12885-024-12791-9.

Supplementary Material 1

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Not applicable.

Author contributions
Y. Liang, Q. Hou, NN. Yao, JT. Liu, and JZ. Cao contributed to the conception and design of the study. Q. Hou, X. Cao, SP. Zhang, LJ. Wei, PX. Feng, and WJ. Zhang organized the database. Y. Liang, Q. Hou, LJ. Wei performed the statistical analysis. Q. Hou, BC. Sun, PX. Feng wrote the first draft of the manuscript. Y. Liang, NN. Yao, JT. Liu and JZ. Cao supervised the project. All authors contributed to manuscript revision, read, and approved the submitted version.

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Data availability
The data from this study are not publicly available to the public for ethical reasons. Data access is, however, possible upon reasonable request to the corresponding authors. All source code has been made publicly available on GitHub at: https://github.com/ilmiss/SCLC_model.

Declarations

Ethics approval and consent to participate
The Authors are responsible for all work respect and ensure that any concerns about the accuracy or integrity of any part of the work are appropriately investigated and addressed. The study followed the 2013 revision of the Declaration of Helsinki and the International Conference on Harmonization's Harmonized Tripartite Guideline for Good Clinical Practice. This study received ethical approval from the Ethics committee of Shanxi Province Cancer Hospital, Shanxi Hospital Affiliated to Cancer Hospital, Chinese Academy of Medical Sciences, Cancer Hospital Affiliated to Shanxi Medical University (No. 202102). The Ethics Committee waived informed consent because it was a retrospective study, and the patients' identities wouldn't be revealed.

Consent for publication
Not applicable.

Competing interests
The authors declare no competing interests.

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